

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 15:42:01 ; Search time 77.81 Seconds

(without alignments)
291.208 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MKKTASQRLFPGPSYONIKS.....LRKCPICRGIKGTVPFLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3277	100.0	618 1	BIR3_HUMAN
2	2728	83.2	612 1	BIR3_MOUSE
3	2353	71.8	604 1	BIR2_HUMAN
4	2233.5	68.2	611 1	BIR.CHICK
5	2172	66.3	600 1	BIR2_MOUSE
6	1532	46.8	358 1	PIAP_PIG
7	911	27.8	497 1	PIAP_HUMAN
8	910	27.8	496 1	BIR4_MOUSE
9	904.5	27.6	496 1	BIR4_MOUSE
10	744.5	22.7	498 1	PIAP2_MOUSE
11	513	15.7	268 1	PIAP2_MOUSE
12	506	15.4	1403 1	BIR2_MOUSE
13	499.5	15.2	1402 1	BIR2_MOUSE
14	498.5	15.2	1402 1	BIR2_MOUSE
15	484	14.8	438 1	PIAP_MOUSE
16	468.5	14.3	1403 1	BIR2_MOUSE
17	468	14.3	1447 1	BIR2_MOUSE
18	462	14.1	1403 1	BIR2_MOUSE
19	461	14.1	275 1	PIAP_MOUSE
20	238.5	7.3	286 1	PIAP_MOUSE
21	237.5	7.2	997 1	BIR1_MOUSE
22	223.5	6.8	275 1	PIAP_MOUSE
23	199.5	6.1	4829 1	BIR6_MOUSE
24	175.5	5.4	239 1	PIAP_MOUSE
25	144	4.4	249 1	PIAP_MOUSE
26	141.5	4.3	142 1	BIR5_MOUSE
27	139	4.2	140 1	BIR5_MOUSE
28	137.5	4.2	236 1	PIAP_MOUSE
29	132.5	4.0	490 1	MDM4_HUMAN
30	131	4.0	142 1	BIR5_MOUSE
31	126	3.8	145 1	PIAP_MOUSE
32	120.5	3.7	834 1	PIAP_MOUSE
33	120.5	3.7	954 1	BIR1_MOUSE

34	119.5	3.6	487 1	MDM2_CANFA
35	119.5	3.6	735 1	YDD7_SCHPO
36	119	3.6	619 1	PIA1_HELPY
37	116.5	3.6	3418 1	BIR2_HUMAN
38	116	3.5	624 1	MDM2_MOUSE
39	115.5	3.5	491 1	MDM2_MOUSE
40	112.5	3.4	1075 1	PST2_MOUSE
41	112.5	3.4	1138 1	PST2_MOUSE
42	109	3.3	619 1	PIA1_HELPY
43	109	3.3	1969 1	PIA1_HELPY
44	109	3.3	2351 1	PIA1_HELPY
45	109	3.3	2469 1	TEGU_HSVSA

ALIGNMENTS

RESULT 1	ID	BIR3_HUMAN	STANDARD	PRT	618 AA.
AC	Q13490	Q16516			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS				
DE	PROTEIN 2) (IAP2) (IAP-2) (C-IAP1) (TNFR2-TRAF SIGNALING COMPLEX				
DE	PROTEIN 2) (IAP2) (IAP-2) (C-IAP1) (TNFR2-TRAF SIGNALING COMPLEX				
GN	BIR3 OR AIP2 OR IAP2 OR MIB.				
OS	Homo sapiens (Human).				
OC	Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;				
OC	Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=66128127; PubMed=8548810;				
RA	Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;				
RT	"The TNFR2-TRAF signaling complex contains two novel proteins related				
RT	to baculoviral inhibitor of apoptosis proteins.";				
RL	Cell 83:1243-1252(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=96149249; PubMed=8552191;				
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertont-Horvat G.,				
RA	Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;				
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related				
RT	family of IAP genes.";				
RL	Nature 379:349-353(1996).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Fetal Liver;				
RX	MEDLINE=96209843; PubMed=8643514;				
RA	Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;				
RT	"Cloning and expression of apoptosis inhibitory protein homologs that				
RT	function to inhibit apoptosis and/or bind tumor necrosis factor				
RT	receptor-associated factors.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).				
RN	[4]				
RP	STRUCTURE BY NMR OF 266-363.				
RA	MEDLINE=99332054; PubMed=10404221;				
RA	Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;				
RT	"Solution structure of a baculoviral inhibitor of apoptosis (IAP)				
RT	repeat.";				
RL	Nat. Struct. Biol. 6:648-651(1999).				
CC	"FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS				
CC	WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO				
CC	FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR				
CC	NECROSIS FACTOR RECEPTOR 2 (TNFR2)."				
CC	"SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL)."				
CC	"TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.				
CC	MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMOUS, TESTIS, OVARY,				
CC	AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD				
CC	LEUKOCYTES."				

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CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: LA9431; AAC41942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR PDB: 1OBH; 20-OCT-99.
DR MTM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR_3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
DR REPEAT 46 113 BIR 1.
DR REPEAT 184 250 BIR 2.
DR REPEAT 269 336 BIR 3.
DR ZN_FING 453 539 CARD.
DR ZN_FING 571 605 RING-TYPE.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
SQ SEQUENCE 618 AA: 69899 MW: C1778D328063586D CRC64;

Query Match 100.0%; Score 3277; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 1,2e-212;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 STSDTTEENADPPIIHGPGSSSEDAVMNMTPVYKSALEKGFNRDLVKOTVOSKILTT 420
QY 421 GENYTVNDIVSALLNAEDEKREKOEKAEEMASDDSLTRKNMMLFOOTCVLPILD 480
DB 421 GENYTVNDIVSALLNAEDEKREKOEKAEEMASDDSLTRKNMMLFOOTCVLPILD 480
QY 481 NLKANVINKEDEHDIKOKTOPIQARELIDTILVKGNAANIFPKCKLEIDSTLYKNLF 540
DB 481 NLKANVINKEDEHDIKOKTOPIQARELIDTILVKGNAANIFPKCKLEIDSTLYKNLF 540
QY 541 VDKNNKXIPTEVSGLSLEQRLRQERTCKVCMDREVSVPFPCGHLVVCQCAPSLR 600
DB 541 VDKNNKXIPTEVSGLSLEQRLRQERTCKVCMDREVSVPFPCGHLVVCQCAPSLR 600
QY 601 KCPICRGIIKGTVPRTFLS 618
DB 601 KCPICRGIIKGTVPRTFLS 618

RESULT 2
BIR3_MOUSE STANDARD: PRT: 612 AA.
ID BIR3_MOUSE
AC 062210; C08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS
DE PROTEIN 2) (MIAP2) (MIAP-2).
CN BIRC3 OR Ap12 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signalling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA MEDLINE=98110590; PubMed=9441758;
RA Lelton P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROOMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: LA9433; AAC42078.1; -
DR EMBL: U88909; AAC53532.1; -
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.

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DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR: 3.
DR Pfam: PF00619; CARD: 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR: 3.
DR SMART: SM00114; CARD: 1.
DR SMART: SM00184; RING: 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD: 1.
KM Apoptosis; Zinc-finger; Repeat.
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 447 525 CARD.
FT ZN_FING 557 591 RING-TYPE.
FT CONFLICT 18 18 N -> Y (IN REF. 4).
FT CONFLICT 119 119 D -> H (IN REF. 2).
FT CONFLICT 153 153 D -> E (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> P (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 364 364 F -> L (IN REF. 2).
FT CONFLICT 352 352 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA: 68371 MW: 8581A00BA9AAB4A7 CRC64;

Query Match 71.8%; Score 2353; DB 1; Length 604;
Best Local Similarity 72.8%; Pred. No. 1,2e-150;
Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

QY 20 SIMEDSTILSDWTNS-NKOKMYDFSCELYRMSTYSTPPAGYVPSERSLARAGFYTGYN 78
DB 2 NIVENSIFLSNLMKSNFELKYLDSCELYRMSTYSTPPAGYVPSERSLARAGFYTGYN 61
QY 79 DAKCCGCCGLMDNKLKGLSPLOKQKOLYPCSCFTIONLYSA-SLSTSKNTSP--MRNSF 135
DB 62 DAKCCGCCGLMDNKLKGLSPLOKQKOLYPCSCFTIONLYSA-SLSTSKNTSP--MRNSF 120
QY 136 AHSLSFTLHSSLSFGSYSSLSPPNLSRAVDISSRTNPNYSYAMSTEARFLYHMMP 195
DB 121 TISLPLGTNSGYFRGYSYNSPNVNSRANODFSALMSSYHCANNENALHFFQYWP 180
QY 196 LTFLSPELRLAGFYIIGPDVACGCGKLSNNEPKDANSEHRRHPNCPLENSL- 254
DB 181 LTFLSPELRLAGFYIIGPDVACGCGKLSNNEPKDANSEHRRHPNCPLENSL- 240
QY 255 ETLRSISLNSQTHAARKTFMYPSSYPVPEOLASGFYVGRNDYKFCDCGGLR 314
DB 241 DTSRYTVSNLSQTHAARKTFMYPSSYPVPEOLASGFYVGRNDYKFCDCGGLR 300
QY 315 CWESGDDPVNAHAKWPFREFLRMGQFVDEIGRYPHLEQLLSTSDTGEENADPP 374
DB 301 CWESGDDPVNAHAKWPFREFLRMGQFVDEIGRYPHLEQLLSTSDTGEENADPP 360
QY 375 IIFGCGESSSDAYMNTPVVKSALWGFNDLVKQVOSKILTTGENYKTVNDIVSL 434
DB 361 IIFGCGESSSDAYMNTPVVKSALWGFNDLVKQVOSKILTTGENYKTVNDIVSL 420
QY 435 LVAEDKREEEKKOEKAEASDLSLRKNRMAFLFOQLTCVPIILDNLKAVINKOEHD 494
DB 421 LVAEDKREEEKKOEKAEASDLSLRKNRMAFLFOQLTCVPIILDNLKAVINKOEHD 480
QY 495 IIKOKTQIPLQARELIDTLVKGNAANIFKMKLEIDSTLVKKNLFVDNMKYPTEDEVS 554
DB 481 VIKOKTQIPLQARELIDTLVKGNAANIFKMKLEIDSTLVKKNLFVDNMKYPTEDEVS 540
QY 555 GLSLEQLRLQLEERTCKVCMKEVSVFIPCGHLVVCQECAPSRLKPCICIGITKTVR 614
DB 541 DLPVEQLRLQLEERTCKVCMKEVSVFIPCGHLVVCQECAPSRLKPCICIGITKTVR 600
QY 615 TFLS 618

DB 601 TFLS 604

RESULT 4
BIR_CHICK STANDARD; PRT; 611 AA.
AC Q90660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN (IAP) (INHIBITOR OF T CELL APOPTOSIS PROTEIN).
GN IFA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT IFA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes.*;
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U27466; AAB48118.1; -;
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR: 3.
DR Pfam: PF00619; CARD: 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR: 3.
DR SMART: SM00114; CARD: 1.
DR SMART: SM00184; RING: 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD: 1.
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT ZN_FING 564 598 RING-TYPE.
SQ SEQUENCE 611 AA: 69009 MW: 53FC9136F34EBDD CRC64;

Query Match 68.2%; Score 2233.5; DB 1; Length 611;
Best Local Similarity 69.2%; Pred. No. 1,3e-142;
Matches 424; Conservative 77; Mismatches 95; Indels 17; Gaps 8;
QY 20 SIMEDSTILSDWTNSNK-NKMYDFSCELYRMSTYSTPPAGYVPSERSLARAGFYTGYN 77
DB 2 NIVENSIFLSNLMKSNFELKYLDSCELYRMSTYSTPPAGYVPSERSLARAGFYTGYN 61

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Db      2 NINDSSPLLAIVKONAHGCELYKDYFSCELYRMSYFSTFPVNVSEBRRLARAGFYTG 61
QY      78 NDKVFCGCGGLMDNMKIKDPSIQRKROLYPCSCFIQMLVSA-SIG-ST-----SKN 127
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      62 QDKVKKFCGGLVDMNQPDNMEKHKOYRSCSFVQMLSLNLGJSTHSATSPVLASN 121
QY      128 TSPRNSFAHSLPTLEHSSLFSGSYSLSPNLSRAVEDISSRTNPYSAMSTPEAR 187
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      122 LSPSLRSM--TLSPSEQVGYFGSGFSFSPBDPVTTRAAPDLSHLRKLQNPMSSTEAR 179
QY      188 FLTYHWWPLTFLSPSELRAGFYTGIPCDRACACGCGKLSNMKPKDASSEHRRHPNC 247
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      180 LRTSHAMPMLCLMPAEVAAAGDDLGTDKVAACVACVKSLSMPEKKNASEHRHPNC 239
QY      248 PPLENSL-ETLRFSISNLSMQTHAARFTFMWSSVVPQPEOLASAFYVGRNDVYC 306
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      240 PVEENLMRQPSFNVSNVMTQTHAARVKTFLMWPRIYVQPEOLADAGFYVGRNDVYC 299
QY      307 FCCDGLRCWESGDDPWVHAHAKFPRCEFLIRMKQGEVNDIGQRYPHLL-EQLSTSDT 365
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      300 FCCDGLRCWESGDDPWVHAHAKFPRCEFLIRMKQGEVNDIGQRYPHLL-EQLSTSDT 359
QY      366 TGEENDAPRIHFGPGESSSEDAVMMNTPVYKSALEMGFNDLYKQTVOSKILTTGENTY 425
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      360 PVDENMD-PIIHFEPESSDEDAIMMNTPVYKAALEMGFNSRLIKQTVOSKILTTGENTY 418
QY      426 TVNDIVSALLNADEKREKEKQAEEMASDLSLIRKRNALFOQLTCVLPILDNLKA 485
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      419 TVNDIVSELLTADEKREKEKQAEEMASDLSLIRKRNALFOQLTCVLPILDNLKA 478
QY      486 NVINKOEHIKOKQIPIQARELIDTLVYGNAANIFKKEIDSTLYKNLFVYKKN 545
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      479 KVTLEHDIKOTYTPQARELIDTLVYKGNMAASIFRNCLEDFPYLKLFEVKS 538
QY      546 KYPTEDVSGSLSEQLRLQERTCKVCMDEKSVVPIPCGHLVYQCECAPSLRKPC 605
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      539 KYPTEDVSGSLSEQLRLQERTCKVCMDEKSVVPIPCGHLVYQCECAPSLRKPC 598
QY      606 RGIKGTVPRTPLS 618
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      599 RGIKGTVPRTPLS 611

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CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC      -----
DR      EMBL: U88908; AAC5331.1; -.
DR      MGD: MGI:1197007; Birc2.
DR      InterPro: IPR001370; BIR.
DR      InterPro: IPR001315; CARD.
DR      InterPro: IPR001841; Zn_finger.
DR      Pfam: PF00653; BIR_3.
DR      Pfam: PF00619; CARD; 1.
DR      Pfam: PF00097; zf-C3HC4; 1.
DR      SMART: SM00238; BIR_3.
DR      SMART: SM00114; CARD; 1.
DR      SMART: SM00184; RING; 1.
DR      PROSITE: PS01282; BIR_REPEAT_1; 3.
DR      PROSITE: PS0143; BIR_REPEAT_2; 3.
DR      PROSITE: PS50209; CARD; 1.
DR      KEGG: Apoptosis; Zinc-finger; Repeat.
FT      REPEAT 27 94 BIR 1.
FT      REPEAT 167 233 BIR 2.
FT      REPEAT 253 320 BIR 3.
FT      DOMAIN 444 512 CARD.
FT      ZN_FING 553 587 RING-TYPE.
SQ      SEQUENCE 600 AA; 67198 MW; AD7E73E6849317D1 CRC64;

Query Match      66.3%; Score 2172; DB 1; Length 600;
Best Local Similarity 66.7%; Pred. No. 1,7e-138;
Matches 406; Conservative 87; Mismatches 96; Indels 20; Gaps 7;

QY      21 IMEDSTILSDWTNS-NKOKMKYDFSCELYRMSYFSTFPAGVPVSEBSRLARAGFYTGND 79
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MYQDSAFIAKLKMSADTFELKDYFSCELYRLSYSAFPKGVPSSEBSRLARAGFYTGAND 60
QY      80 KYKFCGCGGLMDNMKICDPSIQRKROLYPCSCFIQMLVSA-----SLGSKNTSP 130
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 KYKFCGCGGLMDNMKICDPSIQRKROLYPCSCFIQMLVSAFPKGVPSSEBSRLARAGFYTGAND 120
QY      121 MRNSFAHSLPTLEHSSLFSGSYSLSPNLSRAVEDISSRTNPYSAMSTPEARFLT 190
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 L--SFAS-----ENTGYFGSYSPSPDPVNRANDCPALSTSYHRAAMTERARLIT 173
QY      191 YHMPPLTFLSPSELARAGFYTGCDRVACFACGKLSNMKPKDASSEHRRHPNCPEL 250
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      174 YETWPLSLSPAKLAKAGFYTGCDRVACFACDGKLSNMKPKDASSEHRRHPNCPEL 233
QY      251 EN-SLETLRESISNLSMQTHAARFTFMWSSVVPQPEOLASAGFYVGRNDVYKCC 309
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      234 KDLGASARIVYVSNLSMQTHAARFTFMWSSVVPQPEOLASAGFYVGRNDVYKCC 293
QY      310 DGLRCWESGDDPWVHAHAKFPRCEFLIRMKQGEVNDIGQRYPHLL-EQLSTSDTTEE 369
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      294 DGLRCWESGDDPWVHAHAKFPRCEFLIRMKQGEVNDIGQRYPHLL-EQLSTSDTTEE 353
QY      370 NADPPIHFGPGESSSEDAVMMNTPVYKSALEMGFNDLYKQTVOSKILTTGENTYND 429
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      334 NADAIYHFGPGE--SSEVYVMMSTPVYKALLEGFSRSLVROTVOQIATENGENTVSD 412
QY      430 IVSALLNADEKREKEKQAEEMASDLSLIRKRNALFOQLTCVLPILDNLKANYIN 489
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      413 LVIGLIDAEDEMRQEPQAAEEESDILIRKNNMVLFOHLITCVTPPLUYLLSARAIT 472
QY      490 KOEHDITKOTIPIQARELIDTLVYKGNMAANIFKKEIDSTLYKNLFVYKKNKMYIP 549
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      473 EOCNAVAKQKH-TLOASTLIDTLVYKGNMAATSPFNSRLREIDPALYRDIPOODIRSLP 531

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OY 550 TEPVSLSTLEPDLRLQERFCYCKYCKOMKESVYVITPCGHLYVCOEAPSLRKCPCICRGI 609
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 532 TDIIAALPMEEDLRLQERFCYCKYCKOMKESVYVITPCGHLYVCOEAPSLRKCPCICRGI 591

OY 610 KGTATFELS 618
      |||||
Db 592 KGTATFELS 600

RESULT 6
PIAP_PIG ID PIAP_PIG STANDARD: PRT: 358 AA.
AC 062640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE INHIBITOR OF APOPTOSIS.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98162622; PubMed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Tyklick Induced expression of porcine inhibitor of apoptosis
RT protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U79142; AAC39171.1; -.
DR Interpro: IPR001370; BIR.
DR Interpro: IPR001315; CARD.
DR Interpro: IPR001841; Znf_finger.
DR Pfam: PF00653; BIR_2.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR_2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PSS0209; CARD; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT ZN_FING 311 345 RING-TYPE.
SO SEQUENCE 358 AA; 40977 MW; EB226FA9A6190A4 CRC64;

Query Match 46.8%; Score 1532; DB 1; Length 358;
Best Local Similarity 65.1%; Pred. No. 7,8e-96;
Matches 286; Conservative 38; Mismatches 33; Indels 82; Gaps 2.

OY 181 MSTEAREFLTYHHMPLTFLPSSELARAGEYTYIGPDRVACFACGSKLSNMPKPDAMSEH 240
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MNTCEKRLTLTFQWMPPLTFLPSADLAKAGRYTYIGPDRVACFACGSKLSNMPKPDAMTEH 60

OY 241 RRHPPNCPPLFENSL-ELTRFSISLSMOTHAARKMTFTWYSSVPVPEOLASAGTYVG 239
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Dd		61	LRRFNPNCPLFLGNQLODSRTVNLNSMQTYAAAFKTFCCWMPSPISPVHBPQLASAGFYWG	120
Oy		300	RNDYVKCFCCDGGIGRCWESSDDPMVEHAKEFPCEFLIRMKGOEYDEIQGRTPHLLBOL	359
Dd		121	HSDDVCFCGCCGGJLRCSWGSDDPWEHAKEFPCEFLIRKGOEFYSRWQASYPIHLBOL	180
Oy		360	LSTDSTDTGEENADPPIIHFGPGSSSSDAAMNMTPVVKSALENGFNBLVKQTGVSKILIT	419
Dd		181	LSTDSPNDENAEPP-----	195
Oy		420	TGENKYATINDIVSALLNAEDEKREBEKQAEEMASDDLIRKNRMALFQGLTCVLPIL	479
Dd		196	-----NDLSLIRKNRMALFOHLTCTVLPII	219
Oy		480	DNLKANVINKEOHDITIKOTQIPLQARELIDITLVKKNAANIPNKCLKETDSLTKYML	539
Dd		220	DSLIIARIYSOEHDHVLIKOTQYSLQARELIDILLVKGNTAATIFKNSIQEIIDLPMLYML	279
Oy		540	FVDKMMKIYPEDVSGSLSEBQLRLQEBETCKVCMDKEVSVEFTPCGHLYVCOECARSL	599
Dd		280	FVGQDIKITPEENVSDLMSMEDQLRQDEBTCKVCMDKEVSIFYTPCGHLYVCKDCARSL	339
Oy		600	RKCPICGIITKGIYRTFLS	618
Dd		340	RKCPICRGITKGIYRTFLS	358
RESULT 7				
BtR4_HUMAN				
ID	BtR4_HUMAN	STANDARD:	PRT:	497 AA.
AC	P98170; G9NO14;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BAUOLOVRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)			
DE	(IAP-LIKE PROTEIN) (HILP).			
GN	BIRC4 OR API3 OR IAP3 OR XIAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCHI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=96149249; PubMed=8552191;			
RA	Liston P., Roy N., Tamai K., Lefebvre C., Balrd S., Chertton-Horvat G.,			
RA	Farahani R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G.;			
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes";			
RT	Nature 379:349-353(1996).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Fetal heart;			
RX	MEDLINE=96256286; PubMed=8654366;			
RA	Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., Van Dongen J.L.,			
RA	Gillfillan M.C., Shields H., Hardwick J.M., Thompson C.B.;			
RT	"A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors.";			
RT	EMBO J. 15:2685-2694(1996).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	Graham D.;			
RL	Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	FUNCTION.			
RX	MEDLINE=97373959; PubMed=9230442;			
RA	Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;			
RT	"X-linked IAP is a direct inhibitor of cell-death proteases.";			
RT	Nature 388:300-304(1997).			
CC	-!- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND			
CC	CASPASE-7.			
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.			

```

CC -1- TISSUESPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
CC DR EMBL; U45880; AAC50373.1; -.
CC DR EMBL; U32974; AAC50518.1; -.
CC DR EMBL; AL121601; CAB95312.1; -.
CC DR MIM; 300079; -.
CC DR InterPro; IPR001370; BIR.
CC DR InterPro; IPR001841; Znf_fing.
CC DR Pfam; PF00653; BIR; 3.
CC DR Pfam; PF00097; zf-C3HC4; 1.
CC DR SMART; SMO0238; BIR; 3.
CC DR SMART; SMO0184; RING; 1.
CC DR PROSITE; PS01282; BIR_REPEAT_1; 3.
CC DR PROSITE; PS01443; BIR_REPEAT_2; 3.
CC DR Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor.
CC KW REPEAT 26 93 BIR 1.
CC FT REPEAT 163 230 BIR 2.
CC FT REPEAT 265 330 BIR 3.
CC FT 2N_FING 450 484 RING-TYPE.
CC FT CONFLICT 162 162 S->C (IN REF. 1).
CC FT CONFLICT 423 423 Q->P (IN REF. 2).
CC SEQUENCE 497 AA; 56684 MW; 9039AC16D45EB635 CRC64;

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Query Match	27.88	Score 911	DB 1	Length 497
Best Local Similarity	33.88	Pred. NO. 6e-54		
Matches 205; Conservative	89	Mismatches 163	Indels 150	Gaps 14

[illegible]

```
Db      426 -----:| |  
                  :||  
                  -SSQTSLO-----KEI-----435  
  
OY      552 DVSGLSEFQLRLDEERTCKVCMKREYSVPFCGHLVWCOCAPSLRKCPCIGILG 611  
          |||||||: |:|:::|:|||:|::|:|:|:|:|:  
          +-----STEQFLRIHQERLCKICMDRNALIVPFGSHLYTCQGCAEAVDKCPMCYTITFE 490  
  
OY      612 TVRTFLS 618  
          :| |  
          :| |  
          491 KOKIFMS 497  
  
RESULT 8  
BIR4_MOUSE  
ID BIR4_MOUSE STANDARD; PRT; 496 AA.  
AC Q60989; O08865;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS  
   PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)  
DE (IAP HOMOLOG A) (MIAP3) (MIAP-3).  
GN BIRC4 OR API3 OR XIAP OR AIIPA OR MIHA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxId=10090;
```

RP SEQUENCE FROM N. A.
RC STRAIN-C57BL/6 X CBA: TISSUE-Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls R.L., Vaux D.L.;
RH "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
KT receptor-associated factors.",
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N. A.
RA Farshali R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;

```
CC -i- FUNCION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND  
CC CASPASE-7 (BY SIMILARITY).  
CC -i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
CC -i- SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -i- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
-----  
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CC or send an email to license@sib-stb.ch).  
-----  
DR EMBL; U06842; AAC52594.1; -.  
DR EMBL; U088990; AAB58376.1; -.  
DR MGD; MG1:107572; Birc4.  
DR InterPro; IPRO01370; BIR.  
DR InterPro; IPRO01841; znf_ring.  
DR Pfam; PF00653; BIR; 3.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SMO0236; BIR; 3.  
DR SMART; SMO0184; RING; 1.  
DR PROSITE; PS01282; BIR_REPEAT_1; 3.  
DR PROSITE; PS0143; BIR_REPEAT_2; 3.  
KW Apoptosis; Zinc-finger; Repeat.  
FT REPEAT      26           93       BIR 1.  
FT   REPEAT     163        230       BIR 2.  
FT   REPEAT     264        329       BIR 3.  
FT   ZN_FING    449        483       RING-TYPE.  
FT CONFLICT     208        208       E -> K (IN REF. 2).  
FT CONFLICT     317        317       E -> D (IN REF. 2).
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Query Match	27.8%	Score 910;	DB 1;	Length 496;
Best Local Similarity	32.54%	Pred. No. 7e-54;		
Matches 203;	Conservative 92;	Mismatches 156;	Indels 174;	Gaps 14
FT CONFLICT	322	322	W -> C (IN REF. 2).	
FT CONFLICT	346	346	S -> P (IN REF. 2).	
FT CONFLICT	360	360	S -> P (IN REF. 2).	
FT CONFLICT	388	388	I -> L (IN REF. 2).	
FT CONFLICT	449	449	C -> S (IN REF. 2).	
FT CONFLICT	462	462	V -> F (IN REF. 2).	
FT CONFLICT	468	468	V -> A (IN REF. 2).	
FT CONFLICT	490	490	K -> N (IN REF. 2).	
SEQUENCE	496 AA;	56079 MW;	ECSFAE0799F2CDD8	CRC64;
Query Match	27.8%	Score 910;	DB 1;	Length 496;
Best Local Similarity	32.54%	Pred. No. 7e-54;		
Matches 203;	Conservative 92;	Mismatches 156;	Indels 174;	Gaps 14
OY 27 ILSDMTNSKQMKYDFCELYRMSTYTFEPAGVPYSERSLARAGFYTYGVNDKYCFCC	86			
Db 13 VLAD---TNKDE---EFVEEFNRLLKTFANFPSSSPVASTLARAGFLYGEEDTVQCFCC	66			
OY 87 GLMDNMKLGDPIDKHQOLPSCFQIONLVASLSGTSKNTSPMRNSAHSLSPTLEHS	146			
Db 67 HAADRMQIDGAVSRHRRISPCRFI-----NFYFENGAAQSTNPQIGQ	113			
OY 147 SLFS---GSYSLSPNP-----INSRAVEDISSRTNPYSAMSTEARFLTYM	193			
Db 114 QKSENCQGNRPAPDRPETHADYLRTGTQVVDISQ-IPRPNRPSSEARLKSFPN	172			
OY 194 WP-LTFLSPSELARAGFYIGPDRVACFACGKLSNMBPKDAMSEHRHHPNCPFL--	250			
Db 173 WPDYHLTPRELASGLVYTGADQVQCFCGCKLENPEPCDRAVSEHRHHPNCPFLVGL	232			
OY 251-----ENSLETLPFSISNLMSQTHAAMKRFMTVPSPVPQDQLASA	293			
Db 233 RNANVRSESGVSDRNFPSTNSPR-----NPMALVEAIVTFGTWTS--VNKEDLARA	286			
OY 294 GFYYVGRNDVYKCFCCDGLRCMSESGDDPMVYHAKMFPCEFLIRKMGOFVDEIOGRYP	353			
Db 287 GFYALGEGDKVCFHCGGLTDMKSEDPMBDHAKYRPOCKYLLEDKGEYINNT-----	341			
OY 354 HLEEDLLSTDTTGEENADPPIIHRCGSESSSEDAVMNMTPVYKSALEMGFNRLVYQTV	413			
Db 342 HLTHSLESIGLTAETK-----PSLTKRIDDTIFQNPVYGEAIRMGFSFKDIKIM	392			
OY 414 OSKILTTGENTKTVNDIYSALLNADDERKEEKEQAEEASDLSLIRKNMALFOQLT	473			
Db 393 EEKIQTSSSYSLSEVLADIADVSAQKNTDE-----	424			
OY 474 CVLPILDMILKANVINKQEHDIIOKTOIPLDARELIDTILVKGNAANIFKNCLEIDS	533			
Db 425-----SSQTSIQ-----	431			
OY 534 TLYKNLFPVDMKKYIPTEDVSGLSLEEDQLRLQOEBRTCKVCMDEKESVVFIPCGHLVCO	593			
Db 432-----KQISTEEDQLRRQDEKLCICKDRNIALIVFCGHLHYTCK	471			
OY 594 ECAPSLKRCPIRCGIKGTVFELS	618			
Db 472 QCAEAVDKCPMCYVITFKOKIFMS	496			
RESULT 9				
BIR4_RAT	STANDARD:	PRT:	496 AA.	
AC O9R016;				
DT 20-AUG-2001 (Rel. 40, Created)				
DT 20-AUG-2001 (Rel. 40, Last sequence update)				
DT 20-AUG-2001 (Rel. 40, Last annotation update)				
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS				
DE PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)				
DE (IAP HOMOLOG A) (RIAP3) (RIAP-3).				
OS BIRCA OR API3 OR XIAP.				
OS Rattus norvegicus (Rat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (rlap3) mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND
CC CASPASE-7 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC or send an email to license@isb.sib.ch).

DR EMBL: AB033366; BAA85304.1; .
DR InterPro: IPRO001370; BIR.
DR InterPro: IPRO01841; ZnF_Ring.
DR Pfam: PF00653; BIR_3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR_3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
KW Apoptosis; Zinc-finger; Repeat.
FT *REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 483 RING-TYPE.
SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 27.6%; Score 904.5; DB 1; Length 496;
Best Local Similarity 33.2%; Pred. No. 1.6e-53;
Matches 206; Conservative 86; Mismatches 155; Indels 173; Gaps 15;

OY	33	NSNKOKMYDFSCELIYRMSTYSTPRGACYPVSESLARAGFYTYGVNDKYCFCCGLMIDN	92
Db	16	DTNKDE--EEVEEFNNRLKTPANPPSSPYASTLARAGFLYTGEDGYOCFSCHAAVD	72
OY	93	WKLDSPIQHKOLXPSCSFQLNVASLSGSTSKNTSP-----MNSPAHS	138
Db	73	WOYDSDAAGRRHRISPCRFITNGFFYEN-GAT-OSTSPGIONGOYKSENCVGNNHFA--	128
OY	139	LSPLESHSLFGSGSYSLSPNPILMSRAVEDISSRTNPYSYAMSTEAREFLTYHMMP-LT	197
Db	129	----LDNRSETHAYL-----LTGGVYDLSDF-IYPRNAMCSSEARLKTFQWNPDYA	177
OY	198	FLESSELARAGFYIIGCDRYACFACGCKLSNMWEPKDDAMSEHRHPENCPL-----	250
Db	178	HLSPRELASAGLYTTGIDDYOQCFCGCKGLKNWPECPRAWSEHRRHPNCFVLGRNVN	237
OY	251	-----ENSLETLRFSINLSNOTHAAMRFPMTYPPSSVPQOPEDLASAGFYIV	298
Db	238	RSEGSVSSDRNFNPSTNSPR---NPMAAEYDAITVFETGLWLS--VNKDOLARAGEYAL	291
OY	299	GRNDVYCFCCDDGLRWESGDPPWVBEAKMFPRCEFLIRMKGGEPEDTOGRYPHILEQ	358
Db	292	GEGGKVCYFHCGGLTWKWCSEDPWBCHAKYPCCKYLDDKEGYEYINTI-----HLTHS	346
OY	359	LSTDPTTGEEADNPRTIHFGPGESSSEDVAWMNTPVVKSLALEMGFNRIYKOTVOGKIL	418
Db	347	LGESVVTAEKT-----PSYTKKIIDDTIPGNPWQAIRKGFIKFDKIKTMEEKIQ	397
OY	419	TTCGNYKTVNDIYSALLNAEDEKREEDEKQAEEMASDDLILRKNNMALFOOLTLCVLP	478

Db 398 TSGSNYSLEVLADIIVSAQKDNQSD----- 424
 Qy 479 LDNLKAVINKEHDIITKOTIPLQARELIDITLVKGNANAFKNCLEIDSTLYKN 538
 Db 425 -----SSQTSLO----- 431
 Qy 539 LFVDKMKYIPTEDVSGSLSEOLRLQOEERTCKVCKMDREVSVEFIPGCHLVWCOECAPS 598
 Db 432 -----KQISTEQLRLQOEKLCIKCDNRNIAIVFPGCHLVYCKQCAEA 476
 Qy 599 LKRCPCIGIITKVTRELS 618
 Db 477 VDKPCMCCTVITFKOKIRMS 496

RESULT 10
 IAP2_DROME STANDARD; PRT: 498 AA.
 AC 024307: 024177: 024115: 024149: 09V7G1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE APOPTOSIS 2 INHIBITOR (INHIBITOR OF APOPTOSIS 2) (DIAP2) (DIAP) (IAP
 DE HOMOLOG A) (IAP-LIKE PROTEIN) (DILP).
 GN IAP2 OR ILP OR DIHA OR CG8293.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye imaginal disk;
 RA MEDLINE=96128128; PubMed=8548811;
 RA Hay B.A., Wasserman D.A., Rubin G.M.;
 RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
 RT function to block cell death.";
 RL Cell 83:1253-1262(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertom-Horvat G.,
 RA Farahehi R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";
 RL Nature 379:349-353(1996).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RA MEDLINE=96256286; PubMed=8654366;
 RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
 RA Gilliflilan M.C., Shields H., Hardwick J.M., Thompson C.B.;
 RT "A conserved family of cellular genes related to the baculovirus iap
 RT gene and encoding apoptosis inhibitors.";
 RL EMBO J. 15:2685-2694(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RA ROSS J.L.;
 RL Thesis (1991), Vanderbilt University / Nashville, U.S.A.
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borck D., Borchan M.R., Bouck J., Brookslein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod H.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Teector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 [6]
 RP SEQUENCE OF 17-498 FROM N.A.
 RC TISSUE=Larva;
 RA MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakshin M., Hawkins C.J., Puls K.L., Vaux D.L.;
 RT "Cloning and expression of apoptosis inhibitory protein homologs that
 RT function to inhibit apoptosis and/or bind tumor necrosis factor
 RT receptor-associated factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
 CC HID-DEPENDENT CELL DEATH IN THE EYE.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT
 CC DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: LA9441: AAC41610.1: -;
 DR EMBL: U45881: AAC46988.1: -;
 DR EMBL: U32373: AAC47155.1: -;
 DR EMBL: M96581: -; NOT_ANNOTATED_CDS.
 DR EMBL: AE003808: AAF58095.1: -;
 DR EMBL: U38809: AAB08398.1: -;
 DR Flybase: FBgn0015247: Iap2.
 DR InterPro: FBgn0015247: Iap2.
 DR InterPro: IPR001370: BIR.
 DR InterPro: IPR001841: Znf_Iing.
 DR Pfam: PF00653: BIR: 3.
 DR Pfam: PF00097: zf-C3HC4: 1.
 DR SMART: SM00238: BIR: 3.
 DR SMART: SM00184: RING: 1.
 DR PROSITE: PS01282: BIR_REPEAT_1: 3.
 DR PROSITE: PS0143: BIR_REPEAT_2: 3.
 DR Apoptosis: Zinc-finger: Repeat.
 FT REPEAT 9 76 BIR 1.
 FT REPEAT 113 179 BIR 2.


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OY 533 STLYKNLEFVDKMKRYPTEDVSGLSLEBOLRLQERTCKVCMKEVSVFIPCHLYVC 592
DB 215 -----VADRLCKICLGAEKTYCFVPCGHVAVC 242
OY 593 QBCAPSLKPCICIGIIGKTVRPF 616
DB 243 GKCAAGVTCPCVCRGOLDKAVRMV 266

RESULT 12
BIR_MOUSE
ID BIR_MOUSE STANDARD: PRT: 1403 AA.
AC Q9R016; Q9R029; P81703; 009122; 009121;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1E (NEURONAL APOPTOSIS
INHIBITORY PROTEIN 5)
GN BIRC1E OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX HUANG S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
"the mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts.";
RT Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-129/SV;
RC MEDLINE-9941674; PubMed-10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
Kunkel L.M., Miller W., Dietrich W.F.;
"Comparative sequence analysis of the mouse and human Igm1/SMA
interval.";
RT Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE-97131520; PubMed-8975718;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
Kunkel L.M., Dietrich W.F.;
"Rpe mouse region syntenic for human spinal muscular atrophy lies
within the Igm1 critical interval and contains multiple copies of Naip
exon 5.";
RT Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DB EMBL: AF135492; AAD56764.1; -
DB EMBL: AF131205; AAD56760.1; -
DB EMBL: U66326; AAC52974.1; -
DB MGI: MGI:1298220; Birc1e.
DB InterPro: IPR001370; BIR.
DB Pfam: PF00653; BIR_3.
DB SMART: SM00238; BIR_3.
DB PROSITE: PS01282; BIR_REPEAT_1; 2.
DB PROSITE: PS0143; BIR_REPEAT_2; 3.
DB Apoptosis: Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.

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FT REPEAT 278 345 BIR 3.
FT CONFLICT 92 92 K -> R (IN REF. 1).
FT CONFLICT 144 144 S -> R (IN REF. 1).
FT CONFLICT 242 242 S -> G (IN REF. 2).
FT CONFLICT 472 472 T -> A (IN REF. 2).
FT CONFLICT 516 516 A -> D (IN REF. 2).
FT CONFLICT 521 521 A -> T (IN REF. 2).
FT CONFLICT 533 533 V -> A (IN REF. 2).
FT CONFLICT 538 538 S -> I (IN REF. 2).
FT CONFLICT 1092 1092 E -> D (IN REF. 2).
FT CONFLICT 1129 1129 H -> L (IN REF. 2).
FT CONFLICT 1137 1137 R -> Q (IN REF. 2).
FT CONFLICT 1242 1242 V -> I (IN REF. 2).
FT CONFLICT 1276 1276 D -> N (IN REF. 2).
SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BC42 CRC64;

Query Match 15.4%; Score 506; DB 1; Length 1403;
Best Local Similarity 27.3%; Pred. No. 3.9e-26;
Matches 175; Conservative 73; Mismatches 216; Indels 176; Gaps 27;

OY 14 SYONIKSIMEDSTILSDWTNSKOKMYDFSC-----LYRSTYSTPPAGVPSERS 66
DB 31 AFQVAKSOEEB-----HKERMKKKGFSOMSEAKRLKTFETVDFRSMTP--QE 80

OY 67 LARAGFYTYGVNDKYKCECCGMLDNMKLGDSPIQKHOLYPSCSFIONLYVASISGSK 126
DB 81 MAAGFYHTGVKLVQVCCFCCLILFGNSLRKLPLEHKKLPBEEFLQ---GKDVGNIG 137

OY 127 NTSPMRNSFANSLSPTEHNSLFGSGYSLSPPNLSRAVEDISSPTNPYSAMSTEA 186
DB 138 YDIRVK-----SPEKM-----LBGKARY--HBEA 161

OY 187 RLTTHMPLTF--LSPSLARAGFYTGPDRAVCFACGGKLSNWPBKDDAMSEHRRF 244
DB 162 RLSEFDWPPYVHAGTSRVLASAGFVETGKRQTVQCFSGSLCNWBGDDPKWEHAKMF 221

OY 245 PNCPLEN--SLETLRFSTISNLSMOTHA-----R 272
DB 222 PKCFELQSKKSSSELAQYIQSYEGFVHTGHEFVSWVRRELPMYSAKCNDSVFNDEL 281

OY 273 MRFPMYPPSSVPYQPOLASAGFYVGRNDYKCCCGGGRKCESGDDPVEHAKMFR 332
DB 282 MDMFKMPQESPYPGVAVLRAGFYTGKKDIYKRCSCGCEKKAEGDDPMEDIKFFPE 341

OY 333 CEFLIMKQG-EPVDEIOGRYPHLLLEOLSTSDTGEEN-ADPPIH----- 377
DB 342 CVFLQTLKSSAEVYIPLOSQY-----ALPEATFTRSNHDDAAVHSTVVDLGRSAQW 396

OY 378 FGPGESSSEDA-----VMNTPVYKSAI-----EMGFNRDLVKOTVOSKILTT 420
DB 397 FQEARSLSEQLRDNNTKATFRHMNLPEVSSIGTDHLSCVSIISKISOPVQ-EALTI 455

OY 421 GENYKTYNDIVSALLNAEDEKREEEK---EKQAEBSADDLSLRKNMALFOOLTVLP 477
DB 456 PEVFSNLSNYMC---VEGETSGKTTFLKRAFLMAAGCCPLRYQOLVYLSLSITP 511

OY 478 ILDNLKAVYINKQEHDIKQTOIPLQARELIDTILVKGNAANIRKNCI-KEIDSTLY 536
DB 512 --DQGL-ANICAQ-----LLAGGCISBV---CLASSIIOLOH 544

RESULT 13
BIR_MOUSE
ID BIR_MOUSE STANDARD: PRT: 1403 AA.
AC Q9R016; P81704; 009122; 009121;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)

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Tue Jan 8 08:23:32 2002

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Search completed: January 7, 2002, 16:05:23
Job time: 1402 sec
